

GGCTGCCGG

-120

1

10

20

*

40

50

03

[illegible]

FIG. 1B

Arg Val Thr Val Met Ile Ala Ile Val Trp	160	Val Leu Ser Phe Thr
CGA GTT ACT GTC ATG ATT GCC ATT GTC TGG		GTC CTG TCC TTC ACC
Ile Ser Cys Pro Leu Leu Phe Gly Leu Asn	170	Asn Thr Asp Gln
ATC TCC TGC TGC CCA CTG CTC TTC GGA CTC AAC		AAT ACA GAC CAG
Glu Cys Ile Ile Ala Asn Pro Ala Phe Val	180	Tyr Ser Ser Ile
GAG TGT ATC ATT GCC AAC CCT GCC TTT GTG	190	GTC TAC TCC TCC ATT
Val Ser Phe Tyr Val Pro Phe Ile Val Thr	200	Leu Leu Val Tyr
GTC TCA TTC TAC GTG GTG CCC TTC ATC GTC		CTG CTG TAT ATC
Lys Ile Tyr Ile Val Leu Arg Lys Arg Arg	210	Lys Arg Val Asn Thr
AAA ATC TAC ATC GTC GTC CTC CTC CGG AAG	220	AAG CGG GTC AAC ACC
Lys Arg Ser Ser Arg Ala Phe Arg Arg Ala	230	Leu Thr Pro Leu
AAG CGC AGC AGT CGA CGA GCT TTC AGA GCC		CTG AAC CCA CTC

FIG. 1C

Lys Asp Ala Ala Arg Arg Ala Gln Glu Leu Glu Met Glu Met Leu
 AAG GAT GCT GCC CGC CGA GCT CAG GAG CTG GAA ATG GAG ATG CTG 250

Ser Ser Thr Ser Pro Pro Glu Arg Thr Arg Tyr Ser Pro Ile Pro
 TCA AGC ACC AGC CCC CCA GAG AGG ACC CGG TAT AGC CCC ATC CCT 270

Pro Ser His His Gln Leu Thr Leu Pro Asp Pro Ser His His Gly
 CCC AGT CAC CAC CAG CTC ACT CTC CCT CCT GAT CCA TCC CAC CAC GGC 280

Leu His Ser Asn Pro Asp Ser Pro Ala Lys Pro Gly Lys Asn Gly
 CTA CAT AGC AAC CCT CCT GAC AGT CCT GCC GCC AAA CCA GAG AAG AAT GGG 300

His Ala Lys Ile Val Asn Pro Arg Ile Ala Lys Phe Phe Glu Ile
 CAC GCC AAG ATT GTC AAT CCC AGG ATT GCC AAG TTC TTT GAG ATC 310

Gln Thr Met Pro Asn Gly Lys Thr Arg Thr Ser Leu Lys Thr Met
 CAG ACC ATG CCC AAT GGC AAA ACC CGG ACC TCC CTT AAG ACG ATG 330

990

FIG. 1D

Ser Arg Arg Lys Leu Ser Gln Gln Lys Glu Thr Gln
 ACC CGC AGA AAG CTC TCC CAG CAG AAG GAG AAA GCC ACT CAG
 340
 Met Leu Ala Ile Val Leu Gly Val Phe Ile Ile Cys Trp Leu Pro
 ATG CTT GCC ATT GTT CTC CTC GGT GTG TTC TTC ATC ATC TGC TGG CTG CCC
 350
 Phe Phe Ile Thr His Ile Leu Asn Ile His Cys Asp Cys Asn Ile
 TTC TTC ATC ACG CAC ATC CTC CTG AAT ATA CAC CAC TGT GAT TGC AAC ATC
 370
 Pro Pro Val Leu Tyr Ser Ala Phe Thr Trp Trp Leu Gly Tyr Val Asn
 CCA CCA GTC CTC TAC AGC GCC TTC ACA TGG TGG CTG CTG GGC TAT GTC AAC
 380
 Ser Ala Val Asn Pro Ile Ile Tyr Thr Thr Thr Phe Asn Ile Glu Phe
 AGT GCC GTC AAC ACC ATC ATC ATC TAC ACC ACC ACC TTC AAC ATC GAG TTC
 400
 Arg Lys Ala Phe Met Lys Ile Leu His Cys
 CGC AAG GCC TTC ATG AAG ATC TTG CAC TGC TGAGTCTGCCCCCTTGCCTG
 410
 415
 1170
 1264

FIG. 1E

CACAGAGCTGCTTCCACCTCCCTGCCTATGCAGGCCAGACCTCATCCCTGCAAGCTG
TGGCAGAAAGGCCAGATGAACCTTGGCCTTCTCTCGACCCCTGCAGGCCCTGCAGTGTTA
1383
GCTTGGCTCGATGCCCCCTCTCTGCCCCACACACCCCTCATCCTGCCAGGTAAGGCCAGGG
AGACTGGTATCTTACCAGCTCTGGGGTTGGACCCCATGGCTCAGGGCAGCTCACAGAGTGC
1502
CCCTCTCATATCCAGACCCCTGTCTCCTTGGCACCAAGATGCAGCGGCCTTCCTTGACC
TTCCTCTTGGGCACAGAACTAGCTCAGTGGTCGAGCACACCCCTGATCGCTGGCTTGGCC
1621
TGGCCCTTGCCTTGCCCGGATCAGGTGGTGGGAGGGAGCGACACGTTCTTACTTT
ATAGGAACCACATAGGAAAGCAGGGAACACGCCAAGTCCTCCAGGCACATCAGTGTCAAG
1740
AGACACACATAAACACCCAGGTAGCTCCATGGACCCAGAGAACTGAGGCTGAAAAATC
TGTTTCCACTCCAACCTAGTGTGAGTCCCTACTTTTCATAGCCATGGGTATTACTATG
1859

FIG. 1F

TCCTACCTTGTTATAGTATCCCATGGGGTTTCTGTACCATTTGGGGGAAACAACCTCTA
 ATCCTCAAGGGCCCAAGAGAAATCTGTAAAGGAGAAAAATAGGCTGATCTCCCTCTACTCT
 1978
 CCAATCCACTCCACCACTTCTTGATATACCTTGGATGTATCCATTCCCTCACAGCAAATG
 CTGGCCAGTCAGGCCCTTGGACCAGTGTGGAGTTGAAGCTGGATGTGGTAACTTGGGGCT
 2097
 CTTTGGGGCTGGGGGGTGTAAACATCGTCTCTCTTCCATATCTCTTCCCTTCCCAGTG
 CCTCTGCCCTTAGAAGAGGCTGTGGATGGGGTGCTGGGACTGCTGATACCATTTGGGCCCTGG
 2216
 CCCTGAATGAGGAGGGGAAGCTGCAGTTTGGAGGGTTCTGGGATCCAACTCTGTAAACAT
 CACTATACCTGTACCAAAACTAAAAACCTTGACAAGAGTCAAAAAA
 2317

FIG. 1G

I

MD...PL...NISWYDDDLERQNW'SRPFNGSEKADRPHYNYAMIITLLIFIIIFGCVNLVCMVAVSREKALQTIITNY
MGP...P...GNDSDFLLTTNGSHV...PDHDTVTEERDEAWVVGMAIIMSVIVLAIIVFGNVLVIITAIKFERLQITVINY
MGSLQ.PQA.GNWSNGTEAPG..GGARATPYSLQVT...LTLVCLAGLL.MLLTVFGNVLVIIAVFTSRATKAPQNL
MDVLS.PGQ.QNNTTSPPAPE..TCGNTTGISDVTVSQV.ITSLIDGTL.IFCAVITGNAGVVAIALERSLQNVANY
MNTSAPPAVSPNITVLAP.....GKGPWQVA.....FIGITIGLL.SLATVITGNLVIISFKVNTETUKVINY
MGACV.VMTDINIS.....SGLDSNATGITAFSMPGWQLALWTAAYLAL.VLVAVMGNATVIWIIILAHQMRIVTINY

III

III

L I V S L A M A D I I V A T L V M P W V V Y L E V G E M F S R I H C D I F V T L D V M C T A S I L N L C A I S I Q R Y T A V A M P M I M T R Y S S K R R
 F I D S L A C A D I V M G I A V M P F G A S H I I M G M N F G N F W C E F W T S I Q V L C V T A S I E T L C V I A V Q R Y I A I T S F K Y Q S L L T K N K A
 F I V S L A S A D I I V A T L V I P F S L A N E V M Q M Y M E G K T W C E I Y A L D V L F C T S S I V H L C A I S I Q R Y W S I T Q A I E N L K R T P R I
 L G S L A V T D I M V S V L V I E M A A L Y Q V L N N W I L G V T C D L F I A L D V L O C T S S I L H L C A I A I Q R Y W A I T D I D I V N K R T P R P R
 F L L S L A C A D I I I G I F S M N L Y T T Y L L M Q I M A L G T L A C D L W L A L D V A S N A S V M N L I I S F Q R Y F S V T R P L S Y R A K R T P R P R A
 F I V N L A I A D I C M A F N A A F N F V Y A S H N I W Y E G R A F C Y F Q N L F P I T A M F V S I V S M T A I A A Q R Y M A I V R P F Q P R L S A P G T R .

IV

V

VTVMIAIVWVISFETISC. PLLFGLNNTD. QNECIIANPAFVVYSSIMSFYVPIVTLVLVYIKITVLVRKRRKRVTNR- (111)
 RMV. ILMVWVSLGTSFIPIQMHYRATH. QKAIDCYHRETCDDFTNOAYALWSSIVSFYPIVWVYVSRVQVAKRQLQKI- (32)
 KAI. JIITVWVISAVISFPIPLISIEKKGG. GGPQPAEPRCEINDQKWYVWSSCIGSFAPOLIMLVYRIYQIAKRTRVP- (137)
 ALT. SLT. MLICGLISIFPMLGWRTPEDR. SDPDACTISKDMGYTYWSTFGAFYIPILMLVLYGRIFRAARFRIPIT- (110)
 ALM. IGLAMLVSEVLWA. PAILFWQYLUGE. RTVLACQCYIQFLSQPIITFGTAMAAFLYPTVMCTIMWRIYRETNRAREL- (137)
 .AV. IAGIMLVALALAF. PQCFYSTITDEGATKCVVAWPEDSGGKMLLLHYHLIVIALIYE. LPQVWVFVMSVIGLTLWRVSPVG- (12) -

IV.

VI

```

-KEKKAQTMDIAIVICMFIIICWLPFFITHIINIHCOCN...IPPMVLYSAFTWLGYNVSA..VNPPIIYTTFNIEFRNAFMKILHC
-KEKALKKTIGIIMGIITILCWLPFFIVNIVHVIQDNL...IPKEVYIILLNWLGYVNSA..PNPIIYCRSP.DFRIAFQEIILCL--(36)
-REKRRTFVIAVVICMFVVCWEPFFEITYTITAVGCS...VPRITFKFFPMEGYCNSS..LNPIVITYLTFNHDFERRAFMKIILCRC--(6)
-REKRTVKTIOIIMGIITILCWLPFFIVALVLPCESSC..HMPITILGAIINWLGYSNL..INPVIYAYENKDFQNAFMKIIKONFCRQ
-KEKKAARTLSAILLAFIVTMTIYNIMVLVSTFCKDC...VRETUWELGYWIGYVNST..LNPMCYALQNKAFRDIFRLIILHOR--(24)
-AKKIFVKTMVIVUVVTEAICWLPYHLYFIIGTFQEDIYCHKFIQQVILALPWIA..MSSTMYNPPIIYCCINHRFSQERLAPRCC--(62)

```

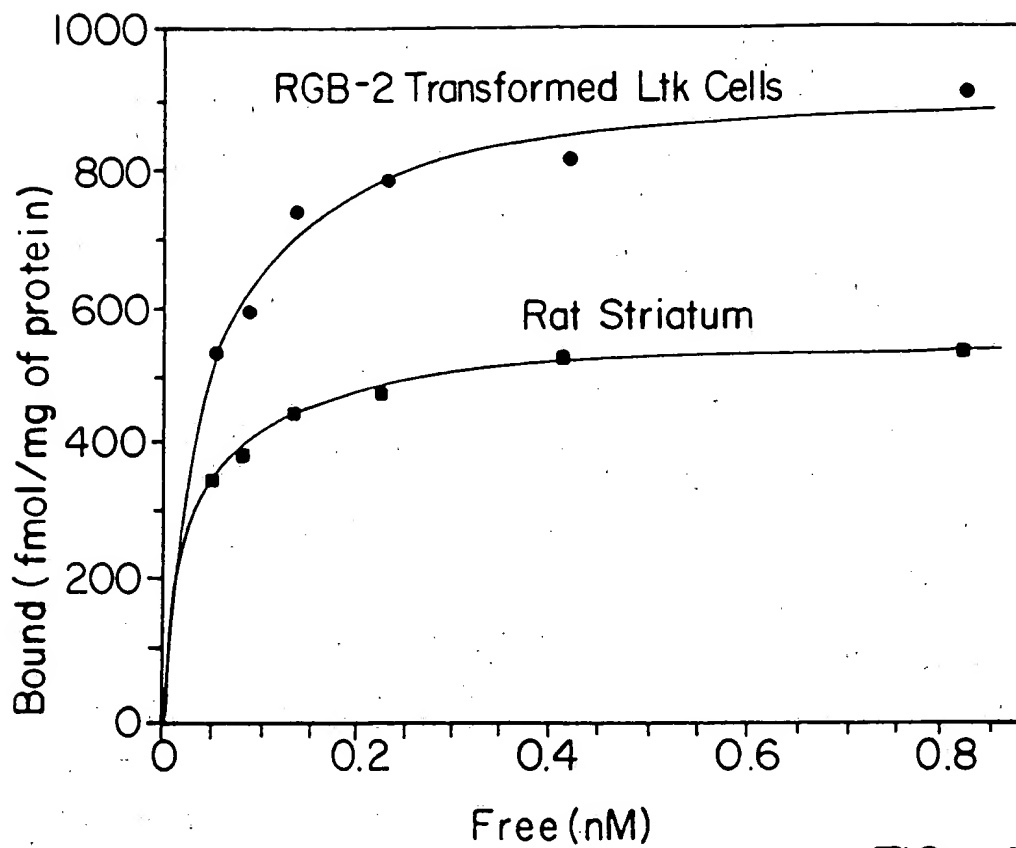



FIG.4A-1

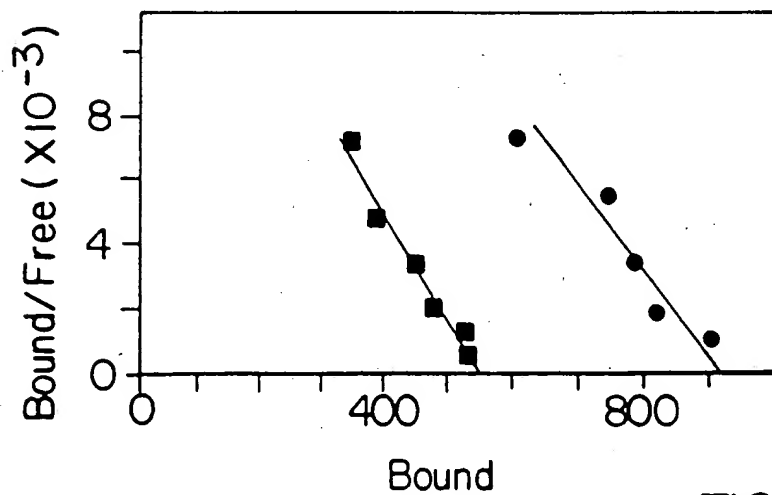
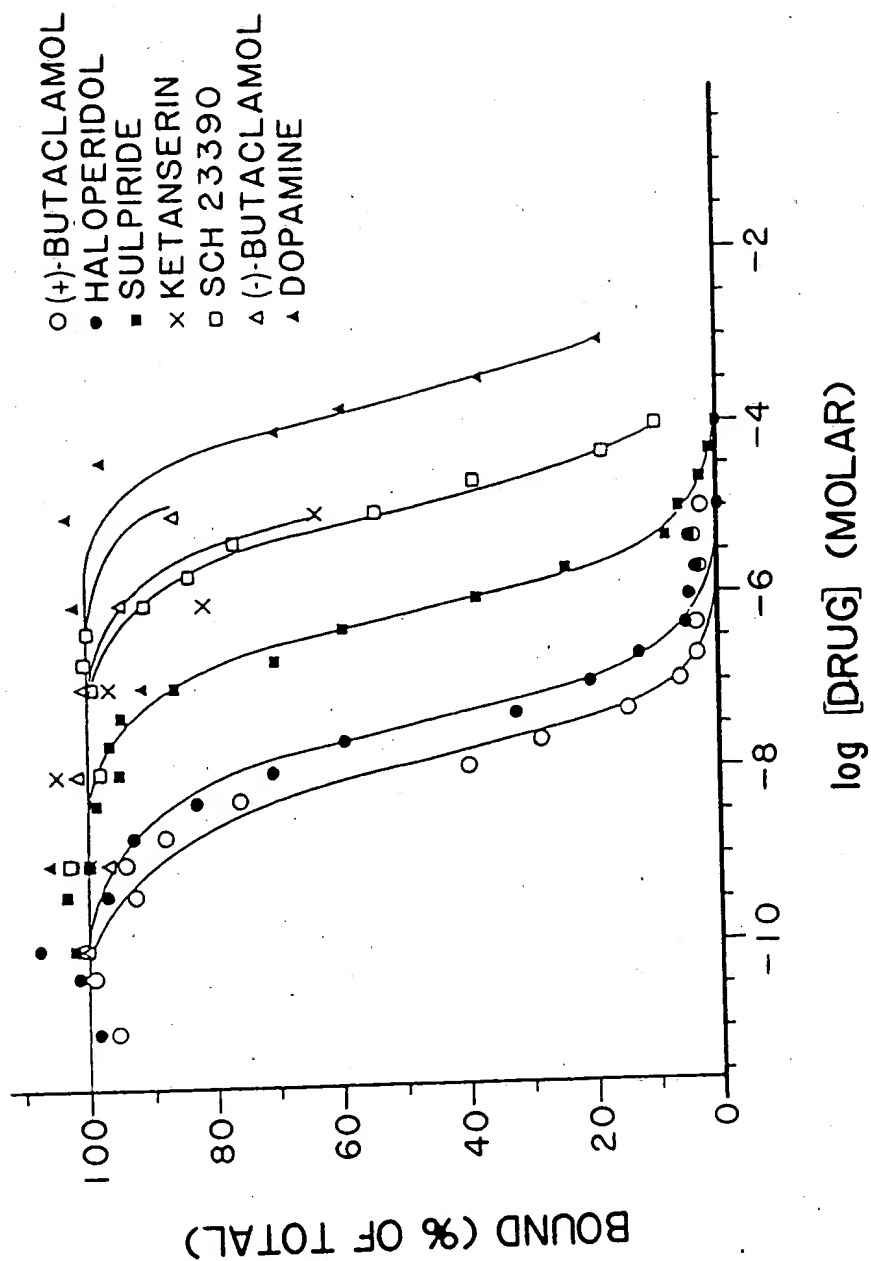


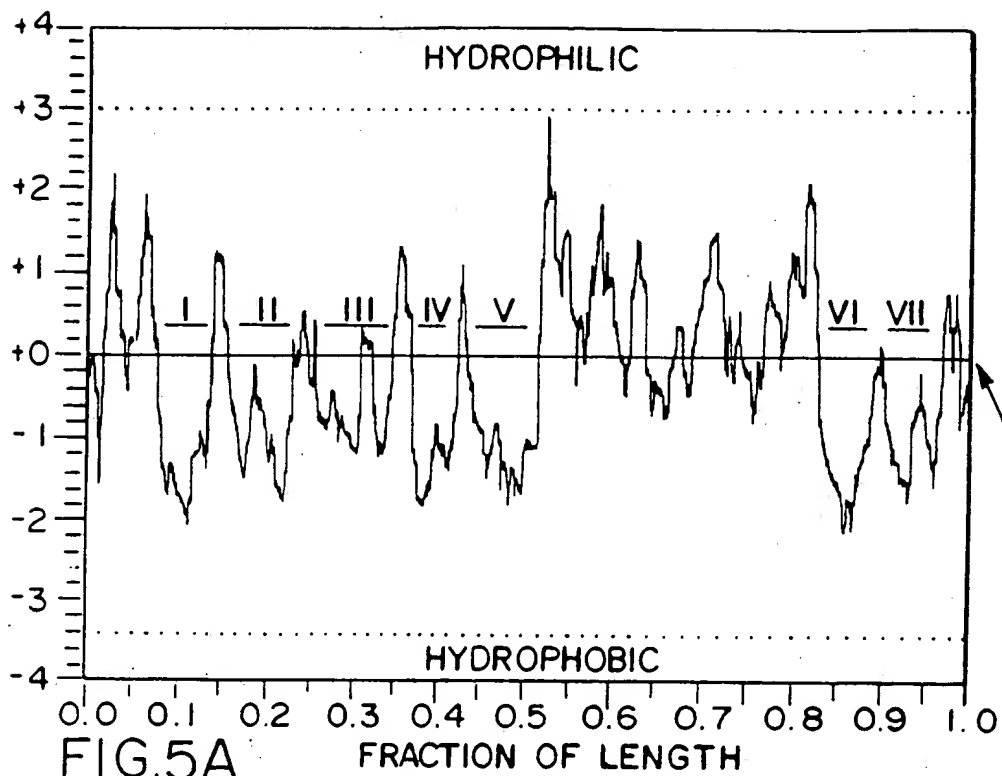
FIG.4A-2

FIG. 4B



DRUG		Ki (nM)	
Transformed Ltk-Cells		Rat Striatum	
RGB-2			
(+)-Butaclamol	0.83	1.0	
(-)-Butaclamol	>1,000	>1,000	
Haloperidol	3.0	5.3	
Dopamine + GTP	17,000	6,300	
Sulpiride			
high affinity	80	67	(87%)
low affinity	---	>10,000	(13%)
SCH 23390			
high affinity	---	35	(16%)
low affinity	1,000	780	(84%)
Ketanserin			
high affinity	---	27	(25%)
low affinity	>1,000	>1,000	(75%)

FIG. 4C



RGB-2

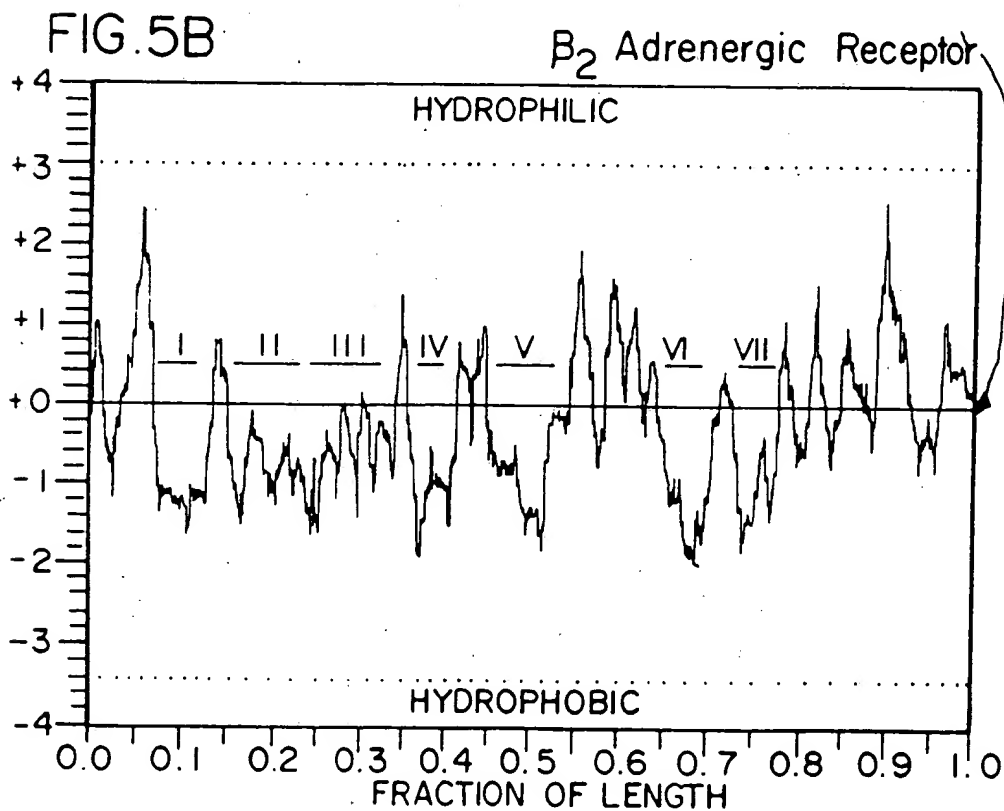
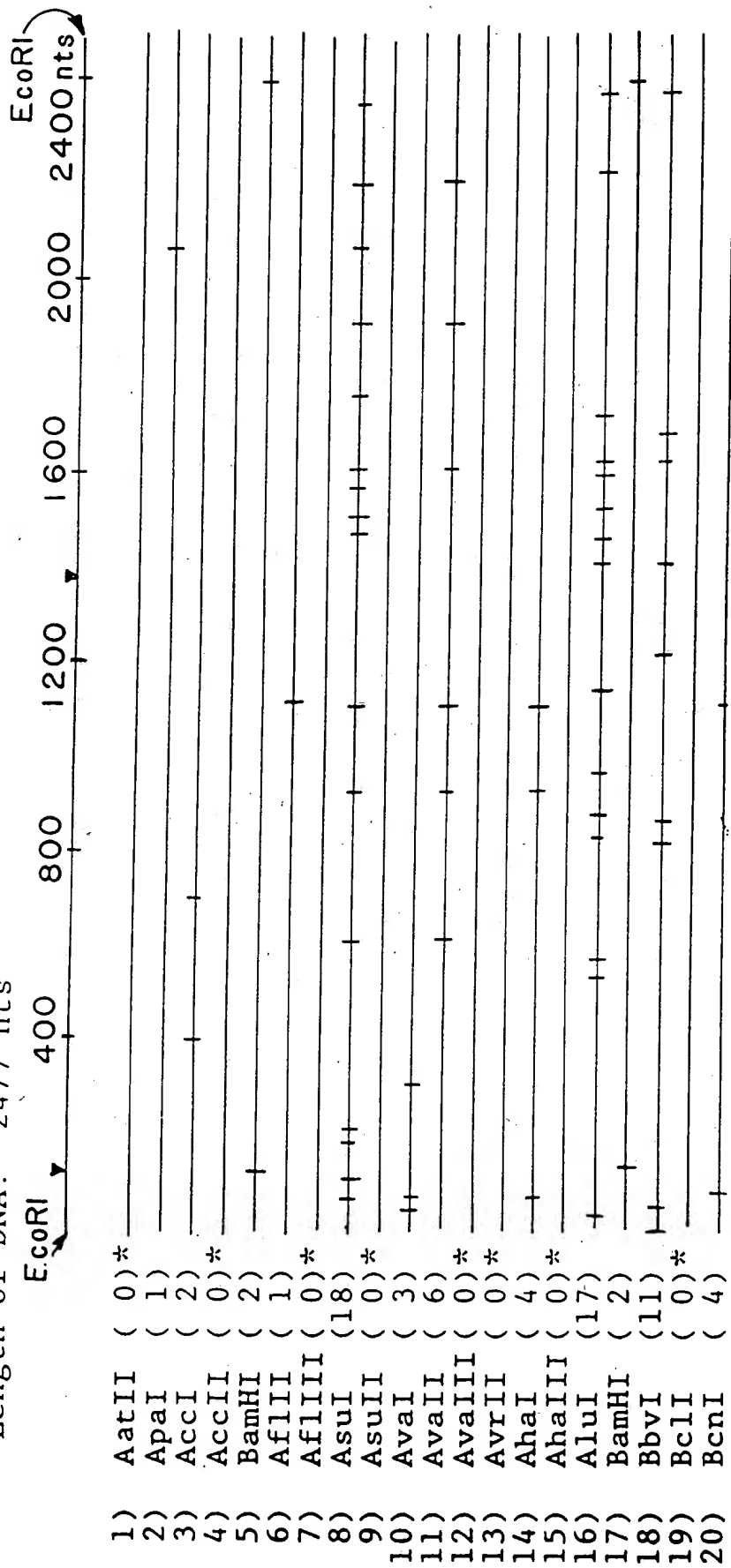


FIG. 6A

Length of DNA: 2477 nts



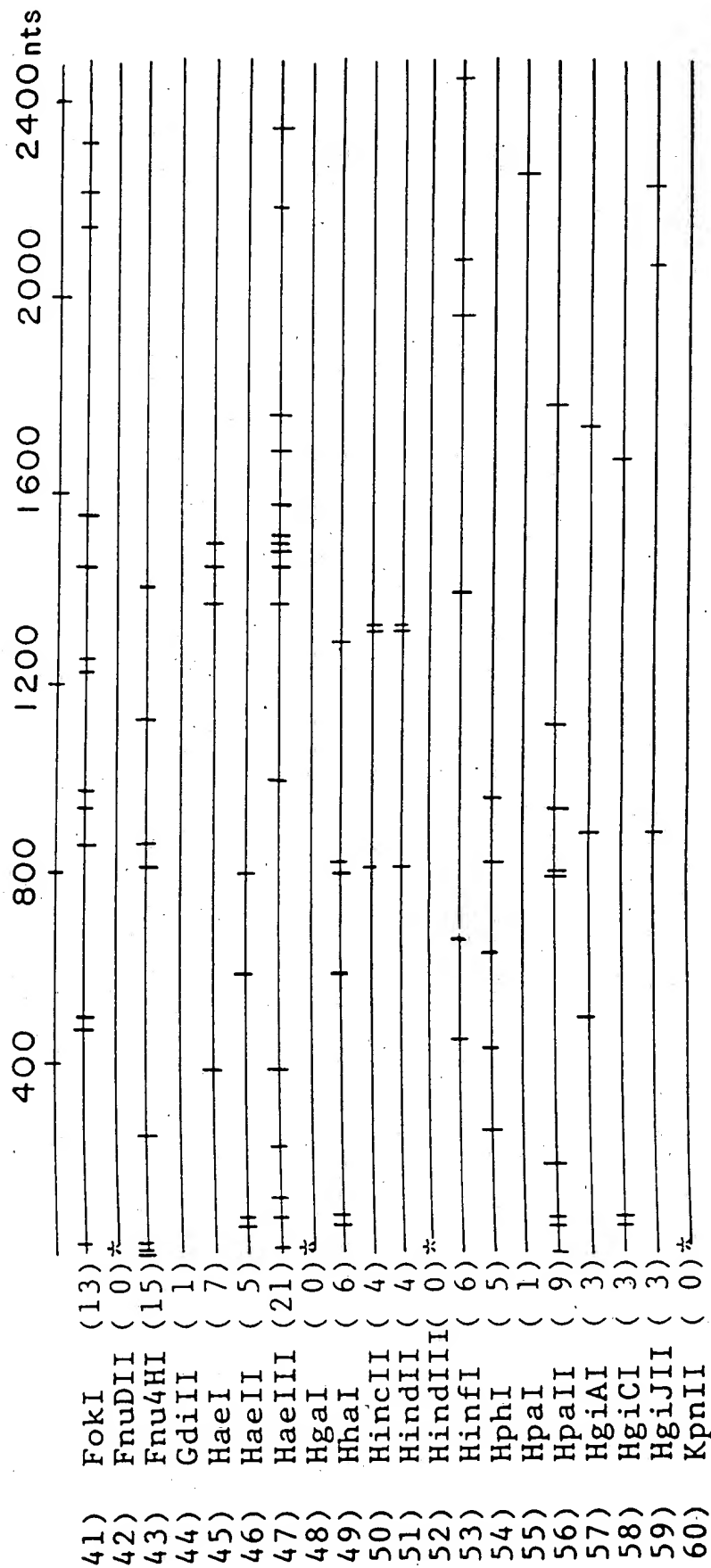


FIG. 6C

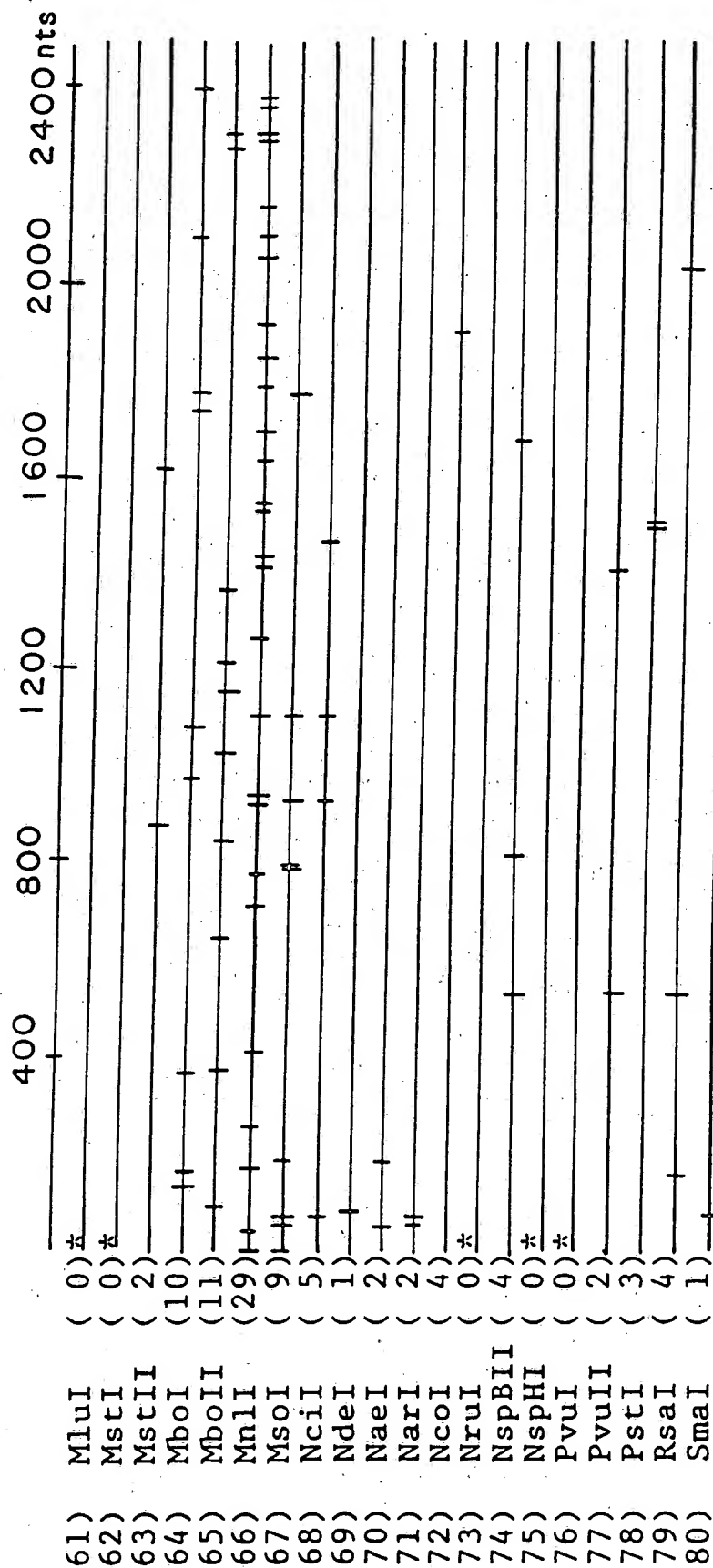


FIG. 6D

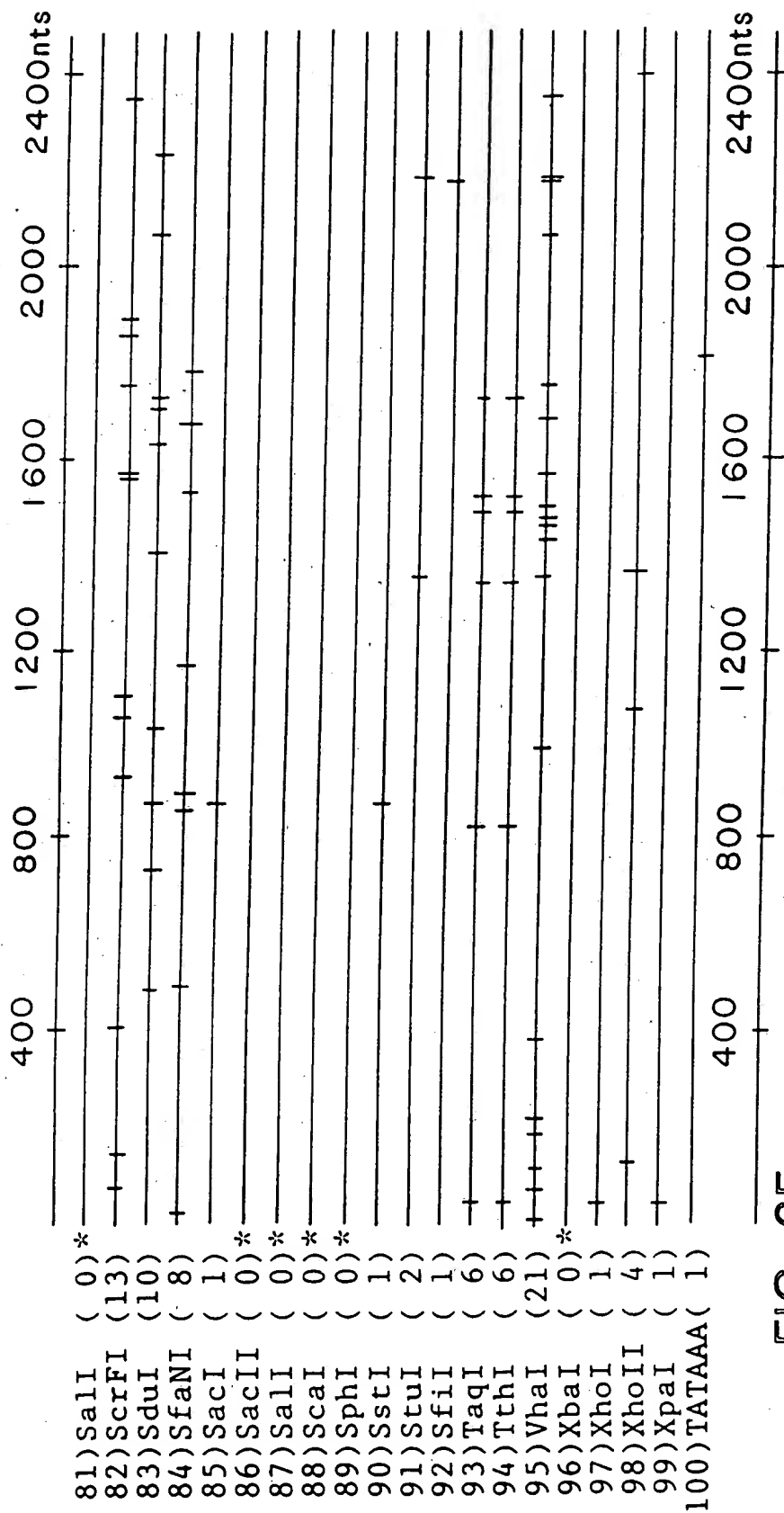


FIG. 6E

[illegible]

81 108

CTG ACA GGG GCT GGG CAG GGT ACC AGA GGT GTC GTG AGG GCT GTC GGG GCG
GAC TCT CCC CGA CCC GTC CCA CCA TGG TCT CCA CAG CAC TCC CGA CAG CCC CGC
Asp Ser Pro Arg Pro Val Pro Pro Trp Ser Pro Gln His Ser Arg Gln Pro Arg
Thr Leu Pro Asp Pro Ser His His Gly Leu His Ser Thr Pro Asp Ser Pro Ala
Leu Ser Pro Thr Arg Pro Thr MET Val Ser Thr Ala Leu Pro Thr Ala Pro Pro

135	162
GTT TGG TCT CTT ACC CGT ACG GTT TTC CTG GTG GGG TTC CTA ACG GTT CTA	
CAA ACC AGA GAA GAA TGG GCA TGC CAA AAG GAC CAC CCC AAG GAT TGC CAA GAT	
Gln Thr Arg Glu Glu Trp Ala Cys Gln Lys Asp His Pro Lys Asp Cys Gln Asp	
Lys Pro Glu Lys Asn Gly His Ala Lys Arg Thr Thr Pro Arg Ile Ala Lys Ile	
Asn Gln. Arg Arg MET Gly MET Pro Lys Gly Pro Pro Gln Gly Leu Pro Arg Ser	

189
GAA ACT CTA GGT CTG GTA CGG GTT ACC GTT TTG GGC CTG GAG GGA GTT CTG GTA
CTT TGA GAT CCA GAC CAT GCC CAA TGG CAA AAC CCG GAC CTC CCT CAA GAC CAT
Leu . Asp Pro Asp His Ala Gln Trp Gln Asn Pro Asp Leu Pro Gln Asp His
Phe Glu Ile Gln Thr MET Pro Asn Gly Lys Thr Arg Thr Ser Leu Lys Thr MET
216

FIG. 7B

CTC GGC ATC CTT C6A G55 GGT CGT CTT CCT CTT TCG GTG AGT CTA CGA GCG	270
GAG CCG TAG GAA G3T C44 CCA GCA GAA GGA GAA AGC CAC TCA GAT GCT CGC	
Glu Pro . Glu C TT Pro Ala Glu Gly Glu Lys Lys Ala Thr Gln MET Leu Ala	
Ser Arg Arg Lys Leu Phe Gln Gln Lys Glu Lys Arg Arg Lys Pro Leu Arg Cys Ser Pro	
Ala Val Gly Ser	
GTA 5CA AGA GCC GCA CAA GTA GTA GAC CGA CGG GAA GAA GTA GTG TGT GTA	324
CAT 4GT TCT CGG CGT GTT CAT CAT CTG CTG GCT GCC CTT CTT CAT CAC ACA CAT	
His T Ser Arg Arg Val His His Leu Leu Ala Ala Leu Leu His His Thr His	
ILE Val Leu Gly Val Phe Ile Ile Cys Trp Leu Pro Phe Phe Ile Thr His Ile	
le Phe Ser Ala Cys Ser Ser Ser Ala Gly Cys Pro Ser Ser Ser His Thr Ser	
GGA CTT GTA TGT GAC ACT GAC GAC GGT GTA GGG CGG ACA GGA CAT GTC GCG GAA GTG	378
CCT GAA CAT ACA CTG TGA CTG CAA CAT CCC GCG TGT CCT GTA CAG CGC CTT CAC	
Pro Glu His Thr Leu . Leu Gln His Pro Ala Cys Pro Val Gln Arg Leu His	
Leu Asn Ile His Cys Asp Cys Asn Ile Pro Pro Val Leu Tyr Ser Ala Phe Thr	
. Thr Tyr Thr Val Thr Ala Thr Ser Arg Leu Ser Cys Thr Ala Pro Ser Arg	
CAC CGA CCC GAT ACA GTT GTC GCG GCA CTT GGG GTA GTA GAT GTG GTG GAA GTT	432
GTG GCT GGG CTA TGT CAA CAG CGC CGT GAA CCC CAT CAT CTA CAC CAC CTT CAA	
Val Ala Gly Leu Cys Gln Gln Arg Arg Glu Pro His His Leu His His Leu Gln	
Trp Leu Gly Tyr Val Asn Ser Ala Val Asn Pro Ile Ile Tyr Thr Thr Phe Asn	
Gly Trp Ala MET Ser Thr Ala Pro . Thr Pro Ser Ser Thr Pro Pro Ser Thr	

459
 GTA ACT CAA GGC GTT CCG GAA GGA CTT CTA GGA GGT GAC GAC TGA GAC GAC GGA 486
 CAT TGA GTT CCG CAA GGC CTT CCT GAA GAT CCT CCA CTG CTG ACT CTG CTG CCT
 His . Val Pro Gln Gly Leu Pro Glu Asp Pro Pro Leu Thr Leu Leu Pro
 Ile Glu Phe Arg Lys Ala Phe Leu Lys Ile Leu His Cys STOPLeu Cys Cys Leu
 Leu Ser Ser Ala Arg Pro Ser . Arg Ser Ser Thr Ala Asp Ser Ala Ala Cys
 513
 CCG CGT GTC GTC GGA CGA AGG GTG GAG GGA CCG GTC ACG GCC GGT CCG AGT GGG 540
 GCC GCA CAG CAG CCT GCT TCC CAC CTC CCT GCC CAG TGC CCG CCA GCC TCA CCC
 Ala Ala Gln Gln Pro Ala Ser His Leu Pro Ala Gln Cys Arg Pro Ala Ser Pro
 Pro His Ser Ser Leu Leu Pro Thr Ser Leu Pro Ser Ala Gly Gln Pro His Pro
 Arg Thr Ala Ala Cys Phe Pro Pro Cys Pro Val Pro Ala Ser Leu Thr Leu
 567
 AAC GCT TGG CAC TCG TCC TTC CCG ACC CAC CTA GCC GGA GGA GAA GAT CGG GGC 594
 TTG CGA ACC GTG AGC AGG AAG GCC TGG GTG GAT CCG CCT CTT CTA GCC CCG
 Leu Arg Thr Val Ser Arg Lys Ala Trp Val Asp Arg Pro Pro Leu Leu Ala Pro
 Cys Glu Pro . Ala Gly Arg Pro Gly Trp Ile Gly Leu Leu Phe . Pro Arg
 Ala Asn Arg Glu Gln Glu Gly Leu Gly Ser Ala Ser Ser Ser Ser Pro Gly

FIG. 7C

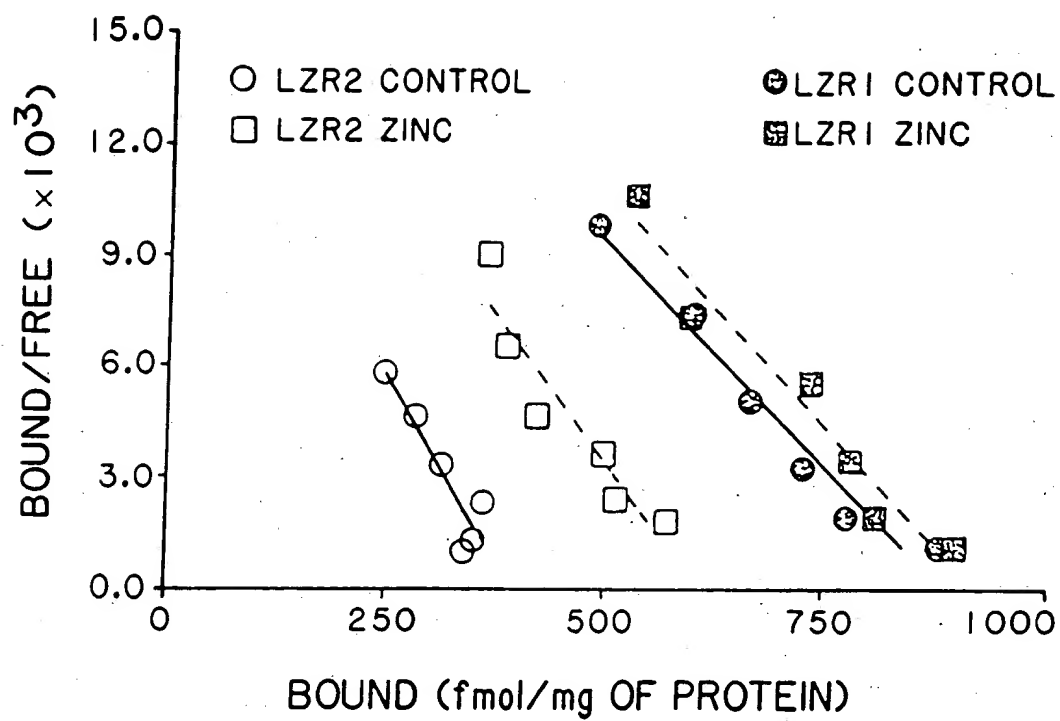


FIG. 8

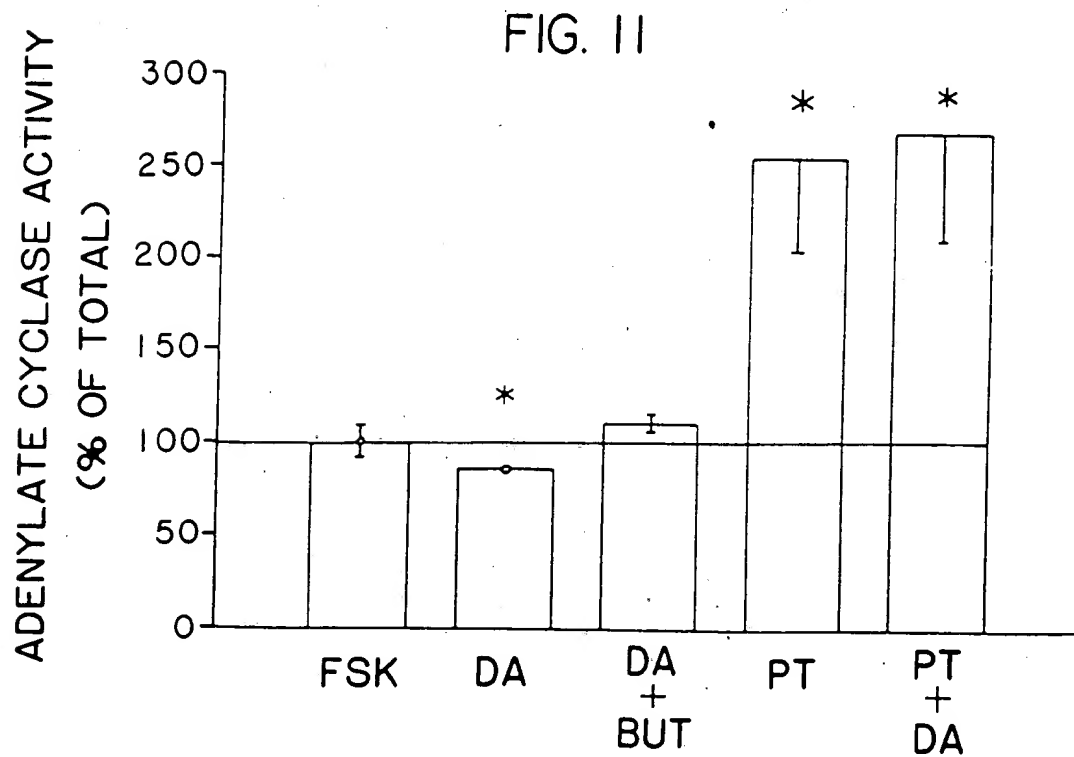


FIG. 9A

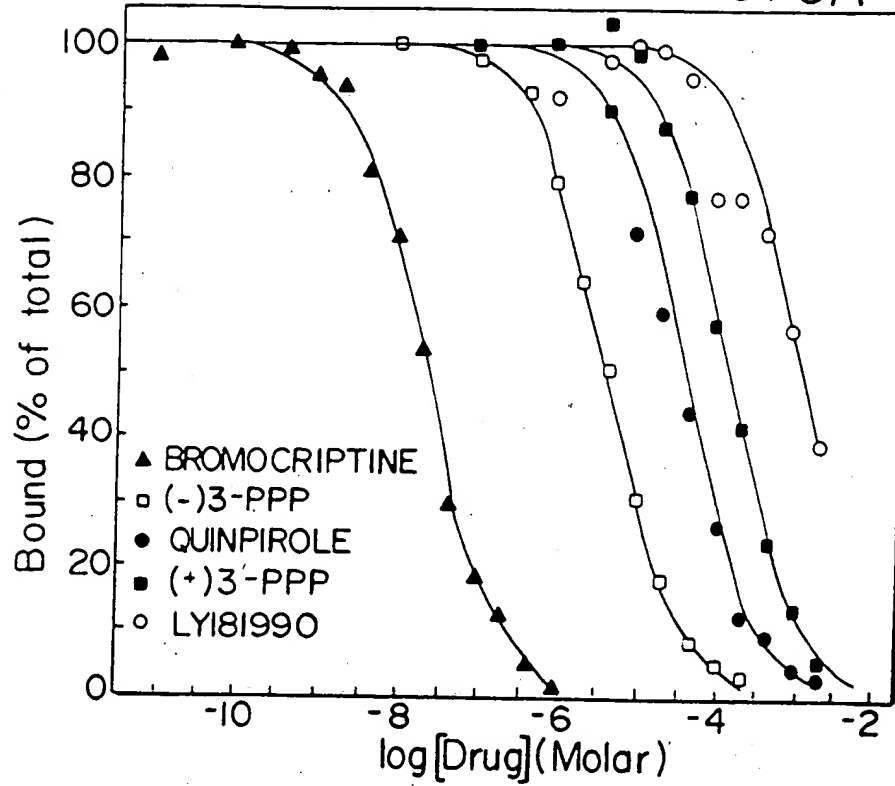
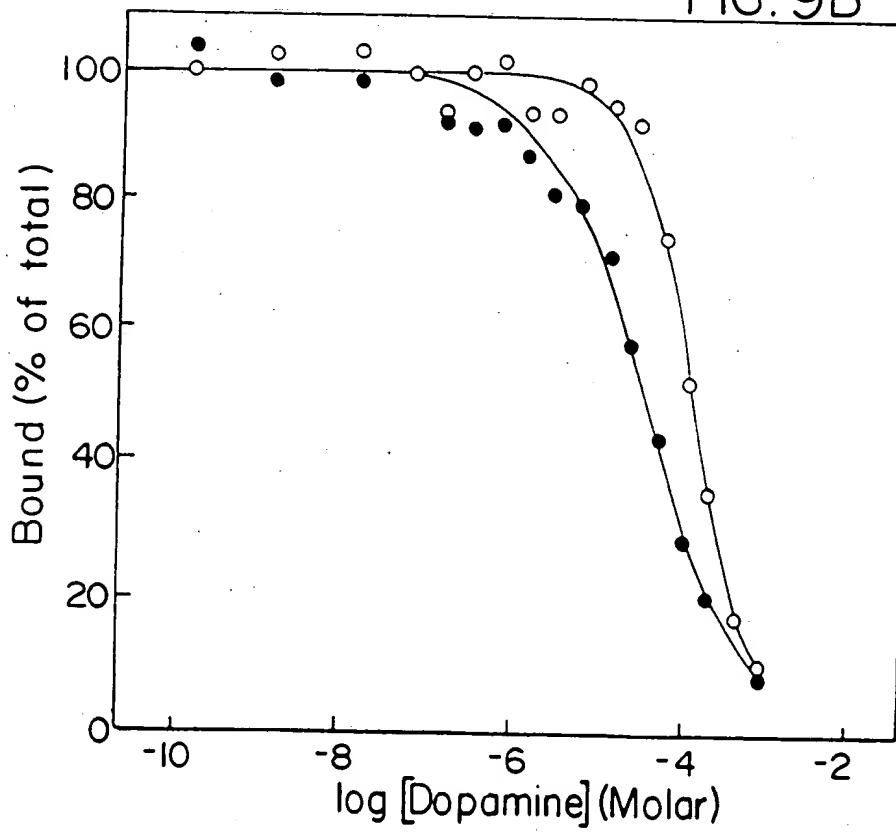
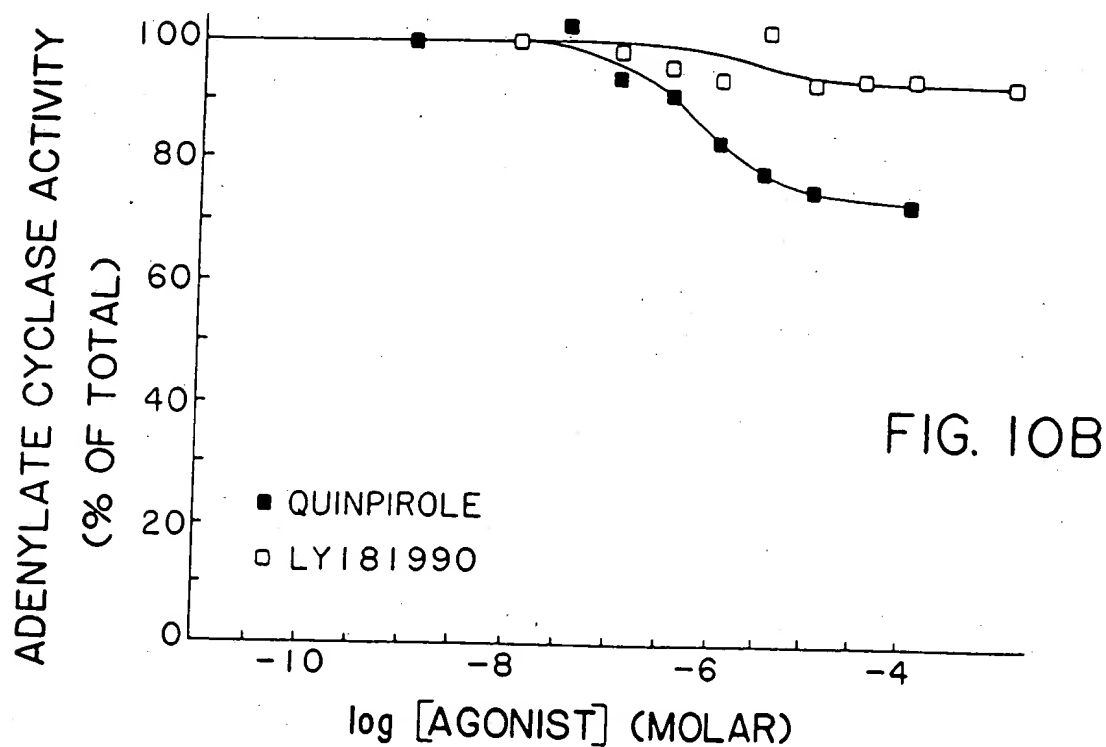
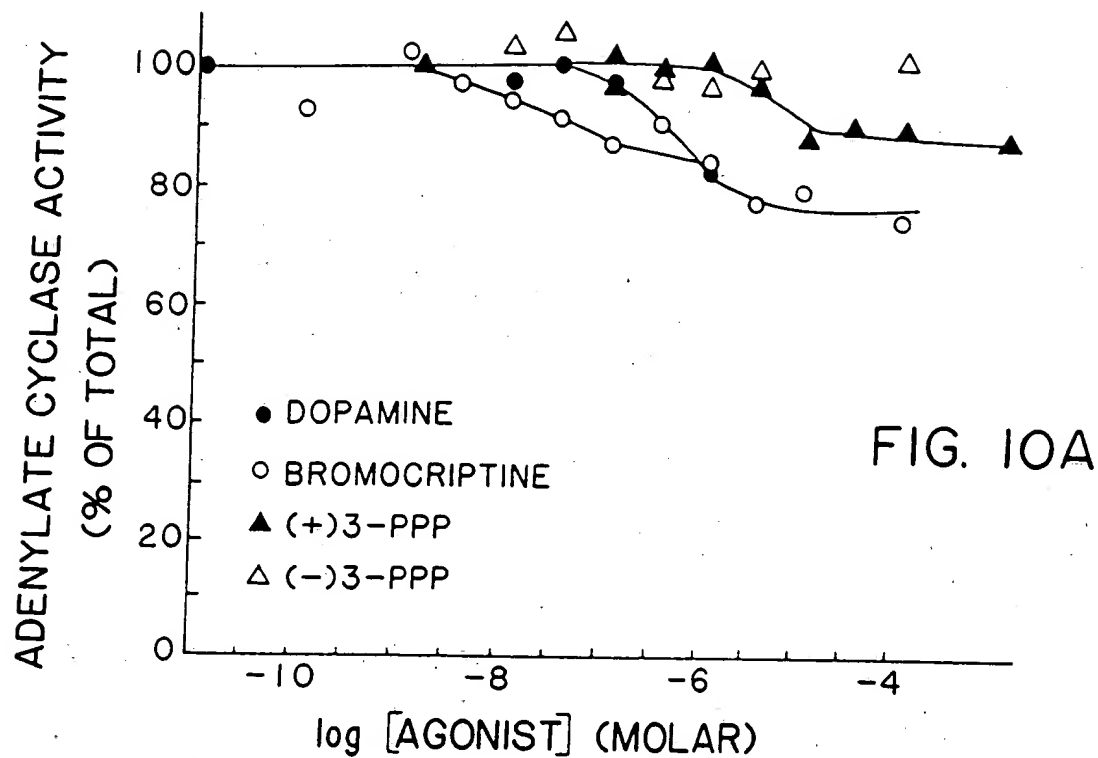


FIG. 9B





CONTROL				+P.T.			
BASAL	FSK	FSK+DA		BASAL	FSK	FSK+DA	
2.1	22.6	14.3		1.7	26.7	23.1	
0.2	2.2	2.1		0.4	2.0	0.5	
—	—	41%		—	—	14%	

FIG. 12A

CONTROL				+P.T.			
BASAL	VIP	DA	VIP+DA	BASAL	VIP	DA	VIP+DA
0.60	2.41	0.32	0.84	0.61	2.68	0.55	2.56
0.02	0.31	0.02	0.13	0.09	0.08	0.03	0.25
—	—	53%	71%	—	—	10%	3%

FIG. 12B

CONTROL				+P.T.			
BASAL	VIP	DA	VIP+DA	BASAL	VIP	DA	VIP+DA
0.78	5.1	0.25	0.76	0.64	5.29	0.66	4.76
0.04	0.4	0.03	0.01	0.01	0.44	0.03	0.16
—	—	68%	88%	—	—	0%	12%

FIG. 12C

123456789101112

FIG. 13B-1

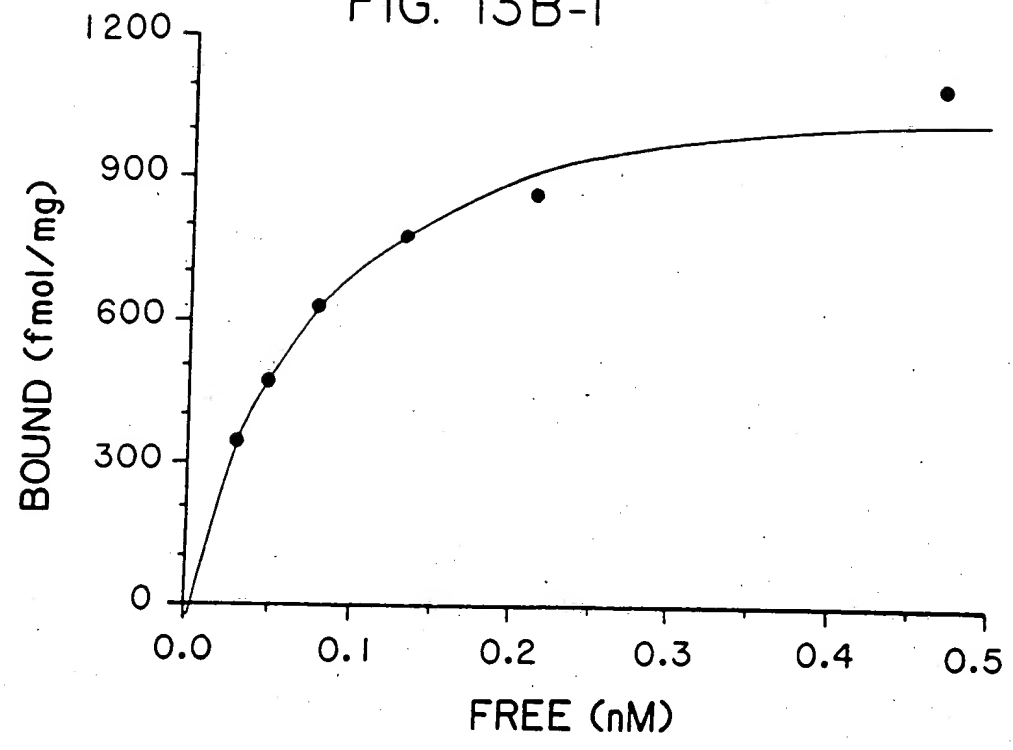


FIG. 13B-2

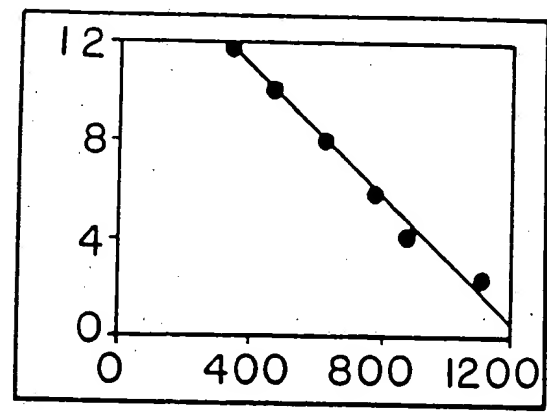
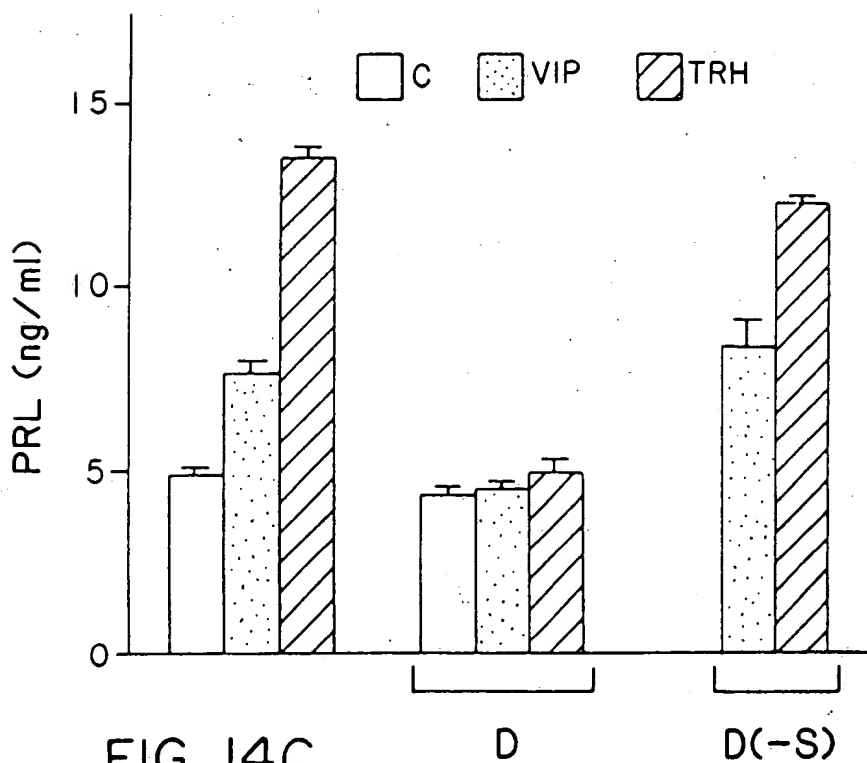
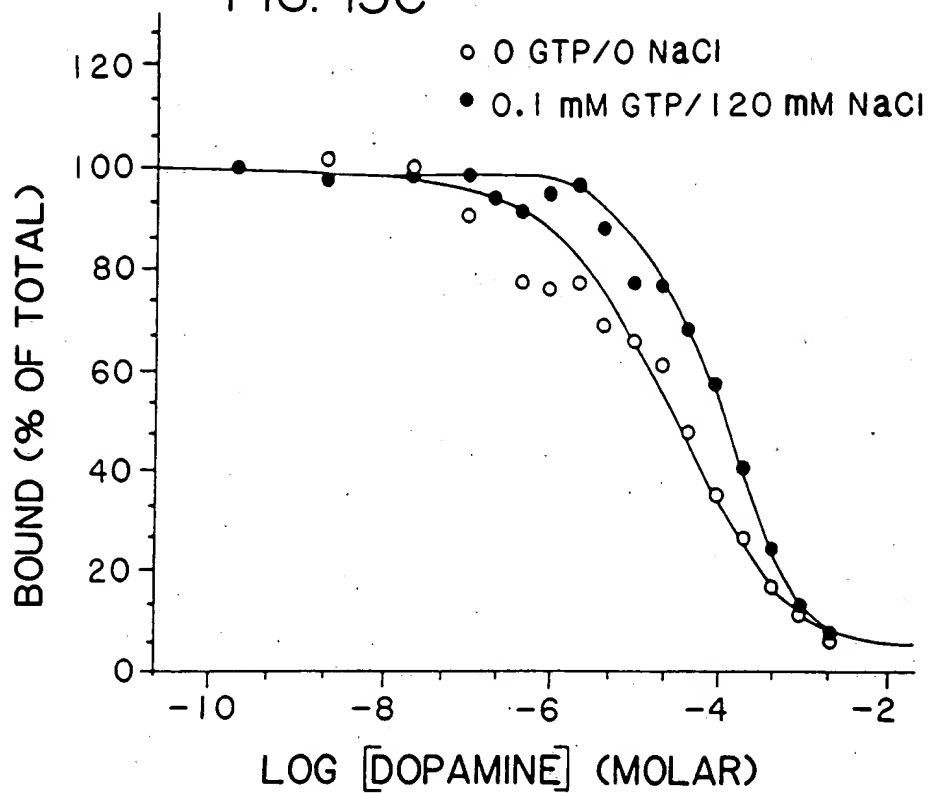


FIG. 13C



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FIG.14A

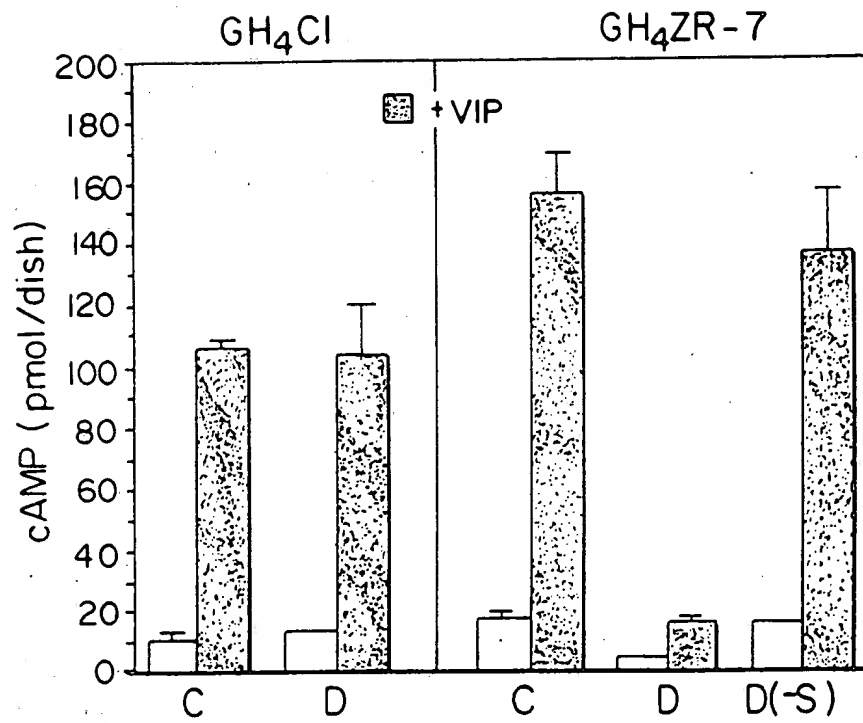
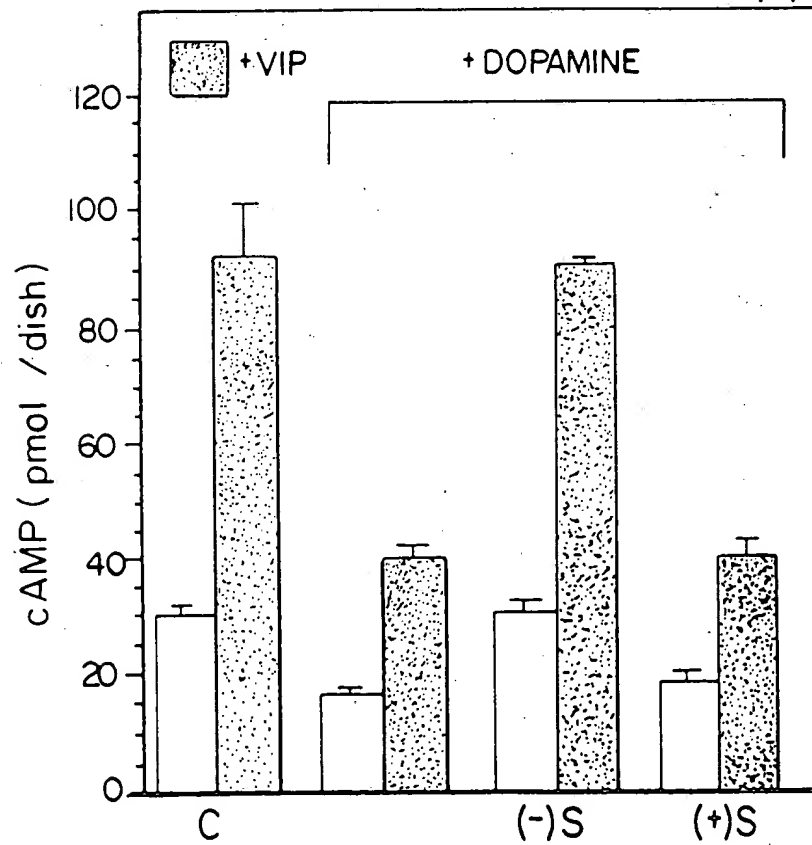


FIG.14B



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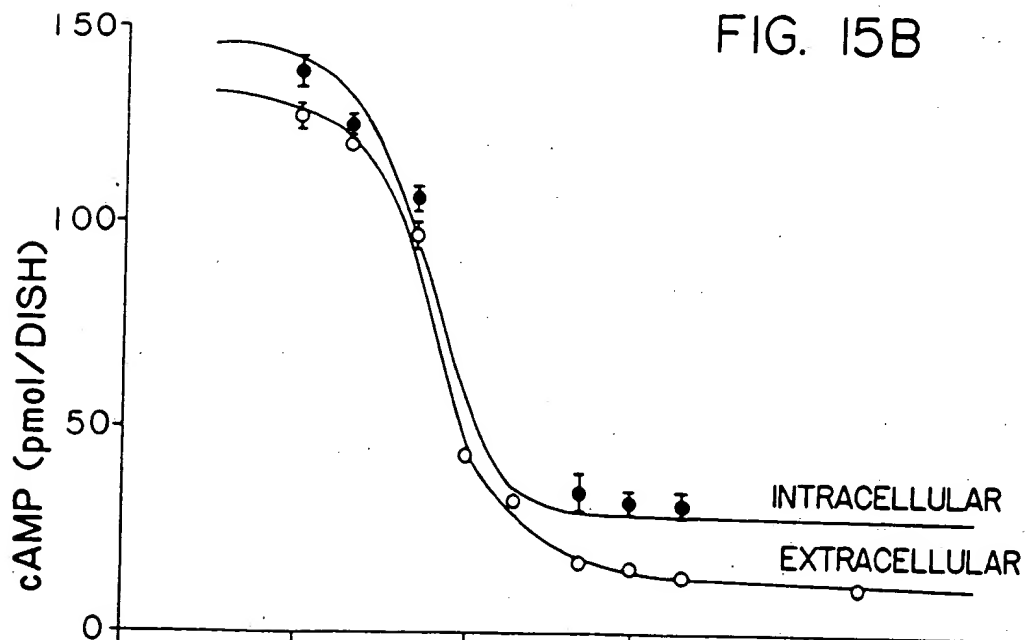
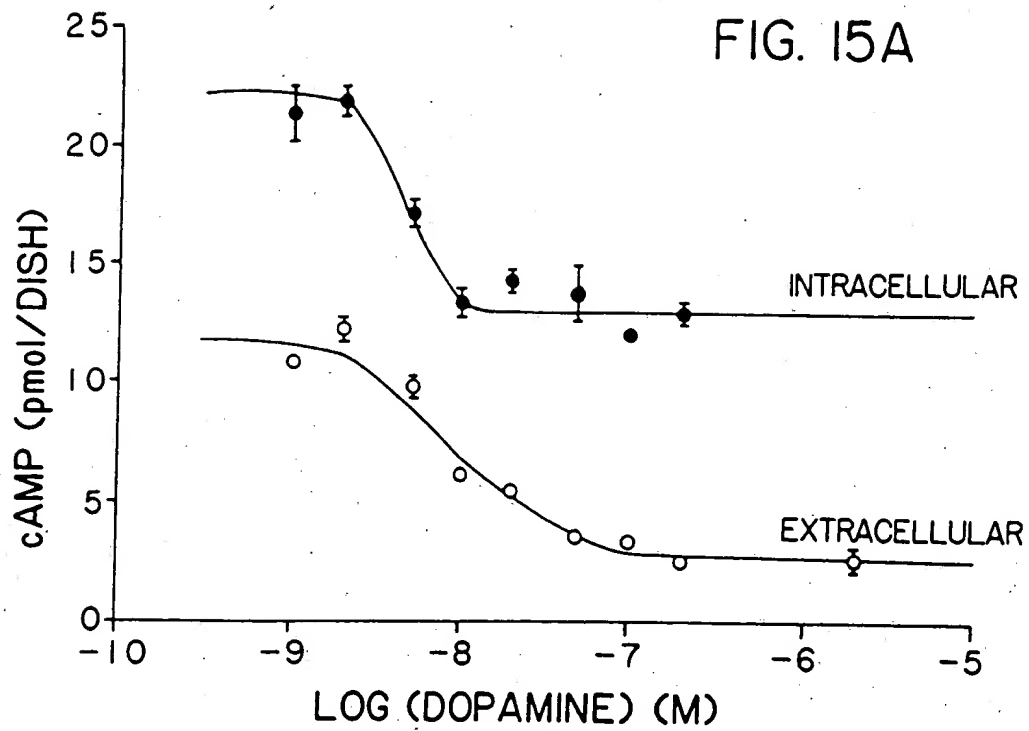


FIG. 16

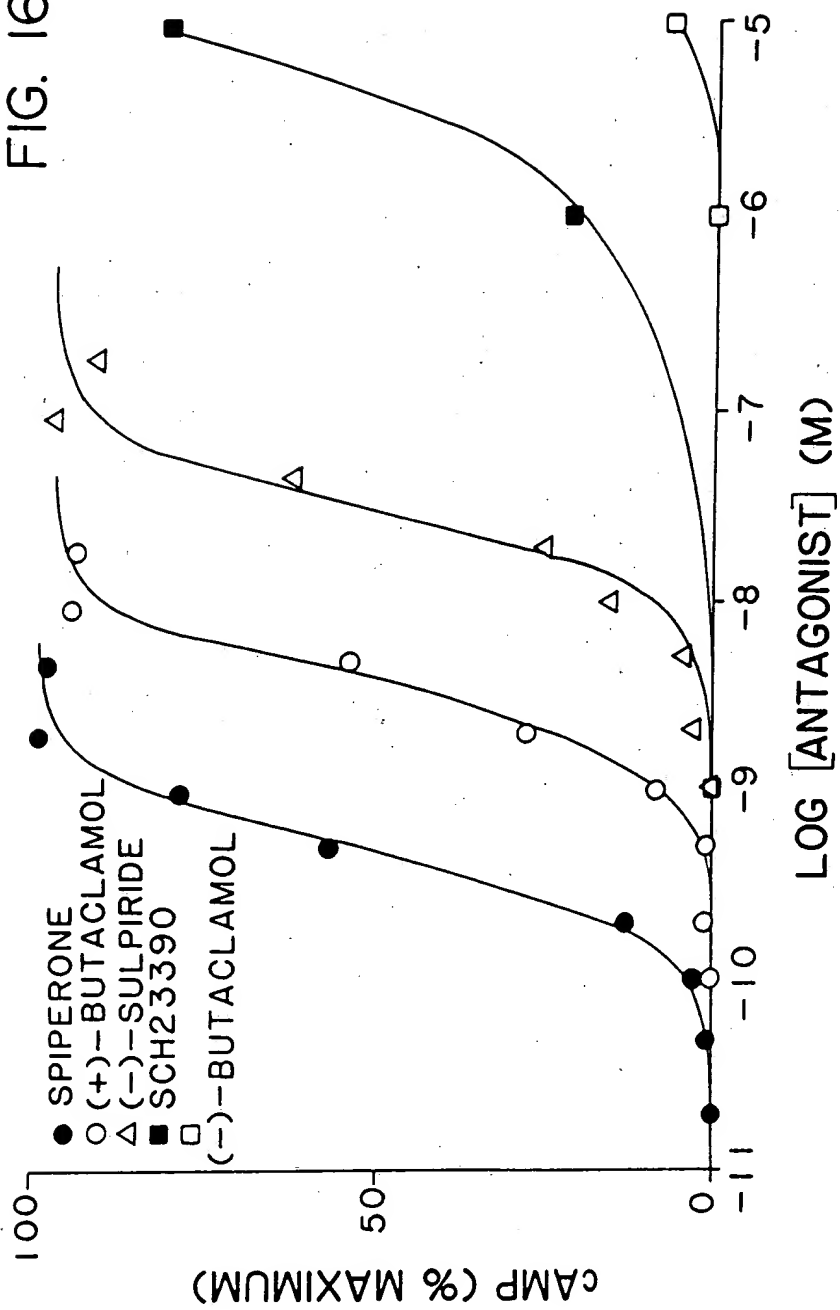


FIG.17A

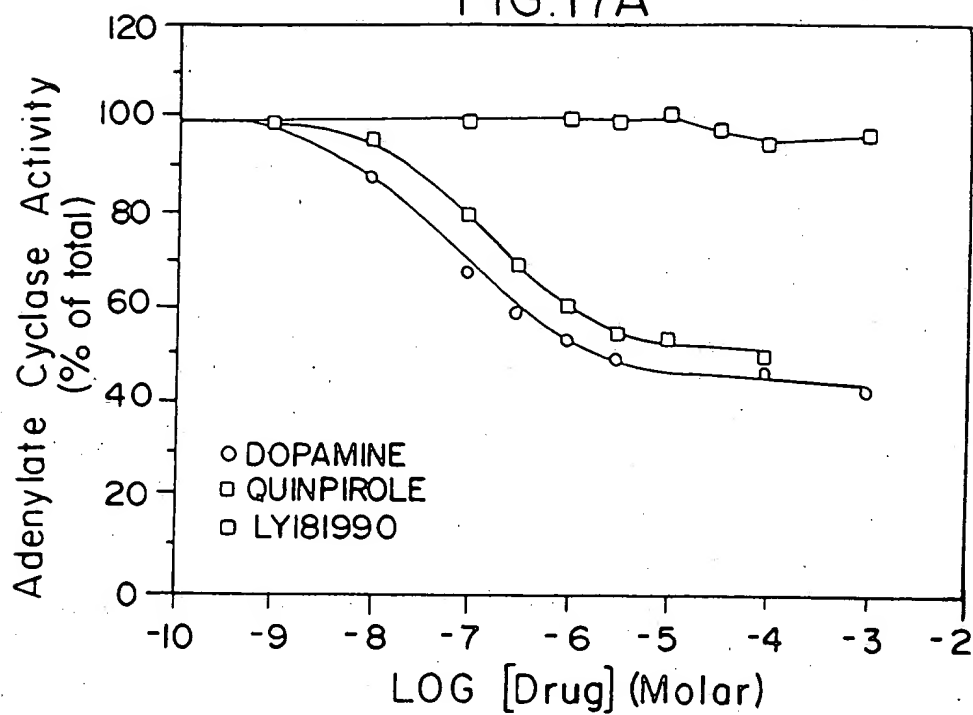
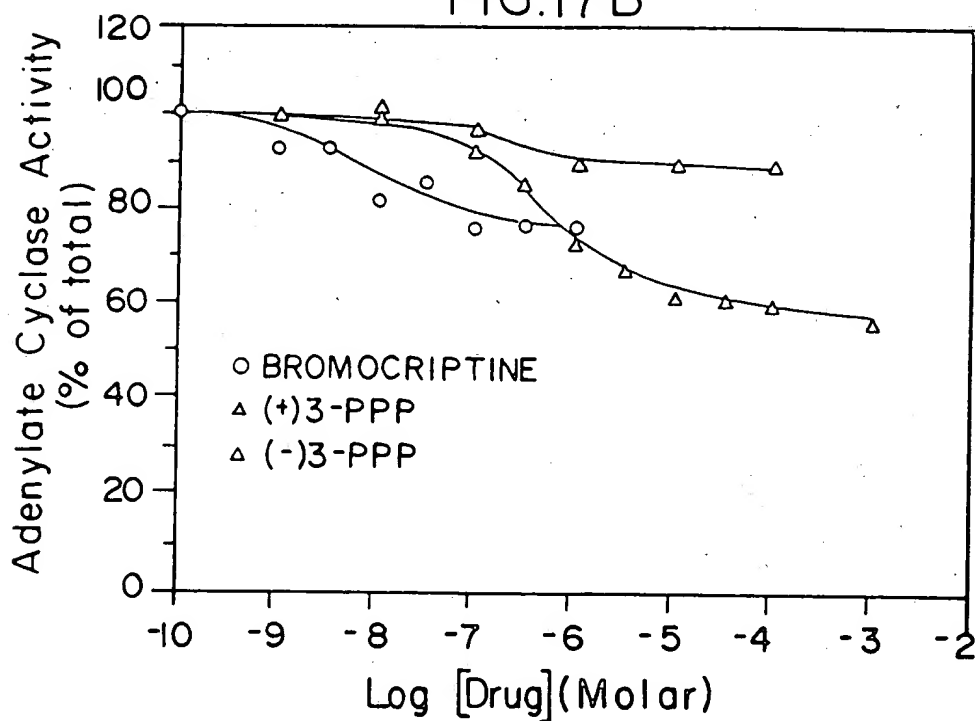


FIG.17B



	1	50	60
LeuThrLeuLeuIleAlaValIleValPheGlyAsnValLeuValCysMETAlaValSer			
CTCACCCCTGCTCATCGCTGTCATCGCTCTTCGGCAACGTGCTGGTGTGCATGGCTGTGTCC			
IIIIIIII			
CTCACCCCTCCTCATCTTTATCATCGTCTTTGGCAATGTGCTGGTGTGCATGGCTGTATCC			
PheIle			
	70	80	
ArgGluLysAlaLeuGlnThrThrThrAsnTyrLeuIleValSerLeuAlaValAlaAsp			
CGCGAGAAAGCGCTGCAGACCAACCACTACCTGATCGTCAGCCTCGCAGTGGCCGAC			
IIIIIIII			
CGAGAGAAAGGCTTTCAGACCAACCACTACTTGATAGTCAGCCTTGCTGTGGCTGAT			240
	90	100	
LeuLeuValAlaThrLeuValMETProTrpValValTyrLeuGluValValGlyGluTrp			
CTCCTCGTCGCCACACTGGTCAATGCCCTGGGTTGTCTACCTGGAGGTGGTAGGTGAGTGG			
IIII			
CTTCTGGTGGCCACACTGGTAATGCCGTGGTGTCTACCTGGAGGTGGTGGGTGAGTGG			

FIG. 18B

[illegible][illegible]

150
 LeuTyrAsnThrArgTyrSerSerLysArgArgValThrValMETIleSerIleValTrp 160
 CTGTACAAATACGGCTACAGCTCCAAGCGCCGGTCACCGTCATGATCTCCATCGTCTGG
 IIIII III IIIIIIIIIIIIIIIII III IIIIIIIII IIIII IIIIIII
 CTGTATAACACACAGCTACAGCTCCAAGCGCCGAGTTACTGTCATGATTGCCATTGTCTGG 480
 Ala

FIG. 18C

IV

ValLeuSerPheThrIleSerCysProLeuLeuPheGlyLeuAsnAsnAlaAspGlnAsn 170 180
 GTCCTGTCCTTCACCATCTCCTGCCCACTCCTCTTCGGACTCAATAACGCAGACCAGAAC
 !!!
 GTCCTGTCCTTCACCATCTCCTGCCCACTGCTCTTCGGACTCAACAATACAGACCAGAAAT
 Thr

GluCysIleIleAlaAsnProAlaPheValValTyrSerSerIleValSerPheTyrVal 190 200
 GAGTGCATCATTTGCCAACCCGGCCTTCGTGGTCTACTCCTCCATCGTCTCCTTCTACGTG
 !!!!!!!
 GAGTGTATCATTTGCCAACCCCTTGTGGTCTACTCCTCCATTTGTCTCATTCTACGTG 600

ProPheIleValThrLeuLeuValTyrIleLysIleTyrIleValLeuArgArgArg 210 220
 CCCTTCATTGTCACCCCTGCTGGTCTACATCAAGATCTACATTGTCTCCGCAGACGCCGC
 !!!
 CCCTTCATCGTCACTCTGCTGCTATATCAAAATCTACATCGTCTCCGGAAGCCCGG
 Lys

FIG. 18D

LysArgValAsnThrLysArgSerArgAlaPheArgAlaHisLeuArgAlaProLeu 230 240
 AAGCGAGTCAACACCAACGCAGCAGCCGAGCTTTCAGGGCCACCTGAGGGCTCCACTA 720
 AAGCGGGTCAACACCAAGCGCAGCAGCTTTCAGAGCCAACCTGAAGACACCACTC
 Asn LysThr
 LysGlyAsnCysThrHisProGluAspMETLysLeuCysThrValIleMETLysSerAsn *
 AAGGGCAACTGTACTCACCCCGAGGACATGAAACTCTGCACCGTTATCATGAAGTCTAAT 250
 !!!
 AAG.....
 GlySerPheProValAsnArgArgValGluAlaAlaArgArgAlaGlnGluLeuGlu 270 280
 GGGAGTTTCCAGTGAACAGCGCGAGAGTGGAGGCTGCCCGGCGAGCCAGGAGCTGGAG
 !!
GATGCTGCCCGCGAGCTCAGGAGCTGGAA 840
 Asp

FIG. 18E

290
 METGluMETLeuSerSerThrSerProProGluArgThrArgTyrSerProIleProPro 300
 ATGGAGATGCTCTCCAGCACCCAGCCCGAGAGGACCCCGTACAGCCCATCCACCCC
 IIIIIIIII IIIIIIIII IIIIIIIII IIIIIIIII IIIIIIIII III
 ATGGAGATGCTCAAGCACCCAGCCCCCAGAGAGGACCCGGTATAGCCCATCCCTCCC
 310
 SerHisHisGlnLeuThrLeuProAspProSerHisHisGlyLeuHisSerThrProAsp 320
 AGCCACCACGCTGACTCTCCCCGACCCGTCCACCATGGTCTCCACAGCACTCCCGAC
 II IIIIIIIII IIIIIIIII III IIIIIII III III III III III 960
 AGTCACCACGCTCACTCTCCCTGATCCATCCACCAACGGCCTACATAGCAACCTGAC
 Asn
 330
 SerProAlaLysProGluLysAsnGlyHisAlaLys AspHisProLysIleAlaLys 339
 AGCCCCGCCAAACCCAGAGAAGAATGGGCATGCCAAA...GACCACCCCAAGATTGCCAAG
 II III IIIIIIIII IIIIIIIII IIIII III III III III III III
 AGTCCTGCCAAACCCAGAGAAGAATGGGCACGCCCAAGATTGTCAATCCACGATTGCCAAG
 IleValAsn Arg

FIG. 18F

IlePheGluIleGlnThrMETProAsnGlyLysThrArgThrSerLeuLysThrMETSer
ATCTTTGAGATCCAGACCATGCCCAATGGCAAACC CGACCTCCCCTCAAGACCATGAGC
TT
TTCTTTGAGATCCAGACCATGCCCAATGGCAAACC CGACCTCCCCTTAAGACCATGAGC
Phe

[illegible][illegible]

FIG. 18G

409 VII 419
AspCysAsnIleProProValLeuTyrSerAlaPheThrTrpLeuGlyTyrValAsnSer

GACTGCAACATCCCGCCTGTCTGTACAGCGCCTTCACGTGGCTGGGCTATGTCAACAGC
 II IIIIIIIIIII II IIIII IIIIIIIIIII IIIIIIIIIIIIIIIIIIIIIIIII
 GATTGCAACATCCACCAAGTCCCTCTACAGCGCCTTCACATGGCTGGGCTATGTCAACAGT

429 439
AlaValAsnProIleIleTyrThrThrPheAsnIleGluPheArgLysAlaPheLeuLys

GCCGTGAACCCCATCATCTACACCACTTCAACATTGAGTTCCGCAAGGCCCTTCCTGAAG
 IIIII IIIIIIIIIIIIIIIIIIIIIIIII IIIIIIIIIIIIIIIIIIIIIIIII 1317
 GCCGTCAACCCCATCATCTACACCACTTCAACATCGAGTTCCGCAAGGCCCTTCATGAAG
 MET

IleLeuHisCys *

ATCCTCCACTGCTGACTCTGCTGCCCTGCCCGCACAGCAGCCTGCTTCCACCTCCCTGCC
 IIII I IIIIIIIIIII
 ATCTTGCACTGCTGA

FIG. 18H

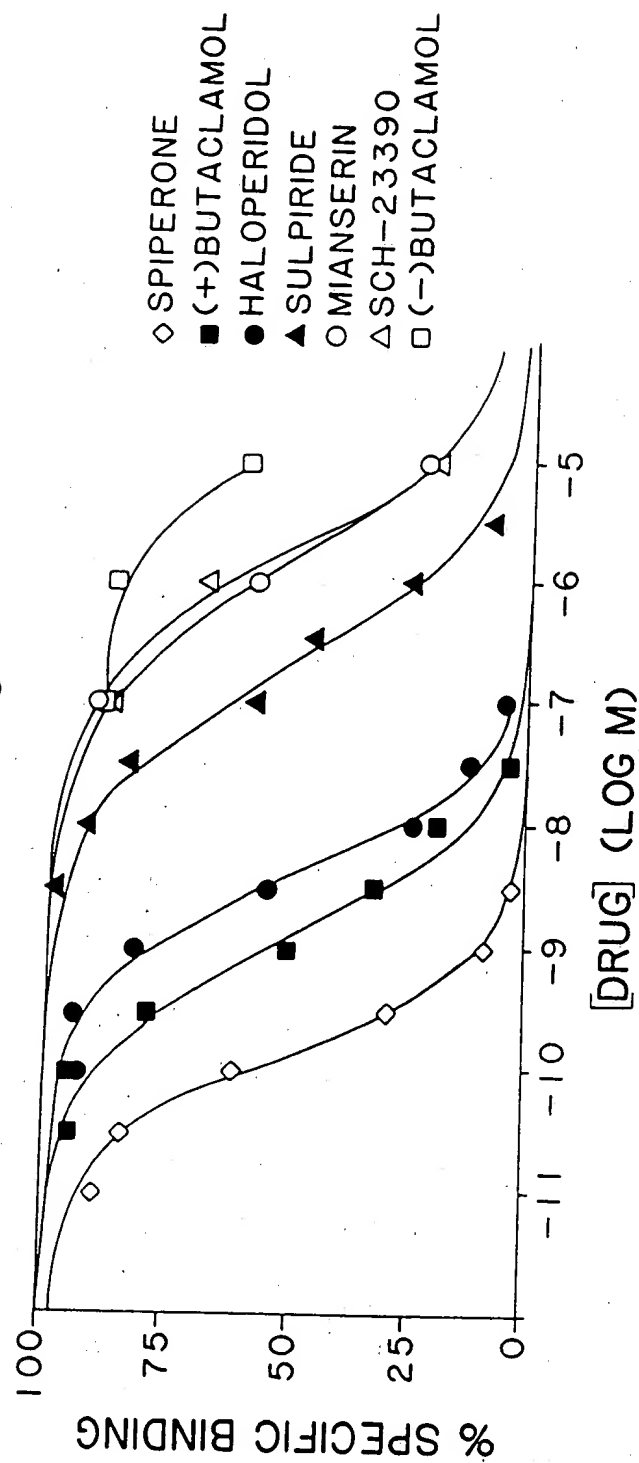
CAGGCCGGCCAGCCTCACCCCTTGCGAACCGTGAGCAGGAAGGCCCTGGGTGGATCGGCCTC 1437
 CTCTTCTTAGCCCCGGCAGGCCCTGCAGTGTTCGCTTGGCTCCATGCTCCTCACTGCCCG
 CACACCCCTCACTCTGCCAGGGCAGTGCTAGTGAGCTGGGCATGGTACCAGCCCTGGGGCT 1557
 GGGCCAGCTCAGGGGCAGCTCATAGAGTCCCCCCTCCACCTCCAGTCCCCCTATCCTT
 GGCACCAAAGATGCAGCGCCCTTCCTTGACCTTCCTCTGGGGCTCTAGGTTGCTGGAGC 1677
 CTGAGTCAGGGCCAGAGGCTGAGTTTCTCTTTGTGGGGCTTGGCGTGGAGCAGCGCGT
 GGGGAGAGATGGACAGTTCACACCCCTGCAAGGCCACAGGAGGCAAGCAAGCTCTCTTGC 1797
 CGAGGAGCCAGGCAACTCAGTCCTGGGAGACCCCATGTAAATACCAGACTGCAGGTTGGA
 CCCCAAGGATTCCCAAGCCAAAACCTTAGCTCCCTCCCGCACCCCGATGTGGACCTCTA 1917

FIG. 18I

CTTCCAGGCTAGTCCGGACCCACCTCACCCCGTTACAGCTCCCCAAGTGGTTTCCACAT
GCTCTGAGAAGAGAGCCCTCATCTTGAAGGGCCAGGAGGGTCTATGGGAGAGGAACT 2037
CCTTGGCCTAGCCACCCCTGCTGCCCTTCTGACGGCCCTGCAATGTATCCCTTCTCACAGC
ACATGCTGGCCAGCCTGGGGCCTGGCAGGAGGTGAGGCCCTGGAACTCTATCTGGGCCT 2157
GGGCTAGGACATCAGAGGTTCTTTGAGGAGTGCCTCTGCCACACTCTGACGCAAACC
ACTTTCCTTTTCTATTCCCTTCTGGCCTTTCCCTCTCTCCTGTTTCCCTTCCCTCCACTGC 2277
CTCTGCCTTAGAGGAGCCACGGCTAAGAGGCTGCTGAAAACCATCTGGCCTGGCCTGGC
CCTGCCCTGAGGAAGGAGGGCAAGCTGCAGCTTGGGAGAGCCCTGGGCCTAGACTCTG 2397
TAACATCACTATCCGATGCACCAAACTAATAAACTTTGACGAGTCACCTTC (A)_n 2449

FIG. 18J

FIG. 19



1 2 3 4

kb

—12.0

— 6.0

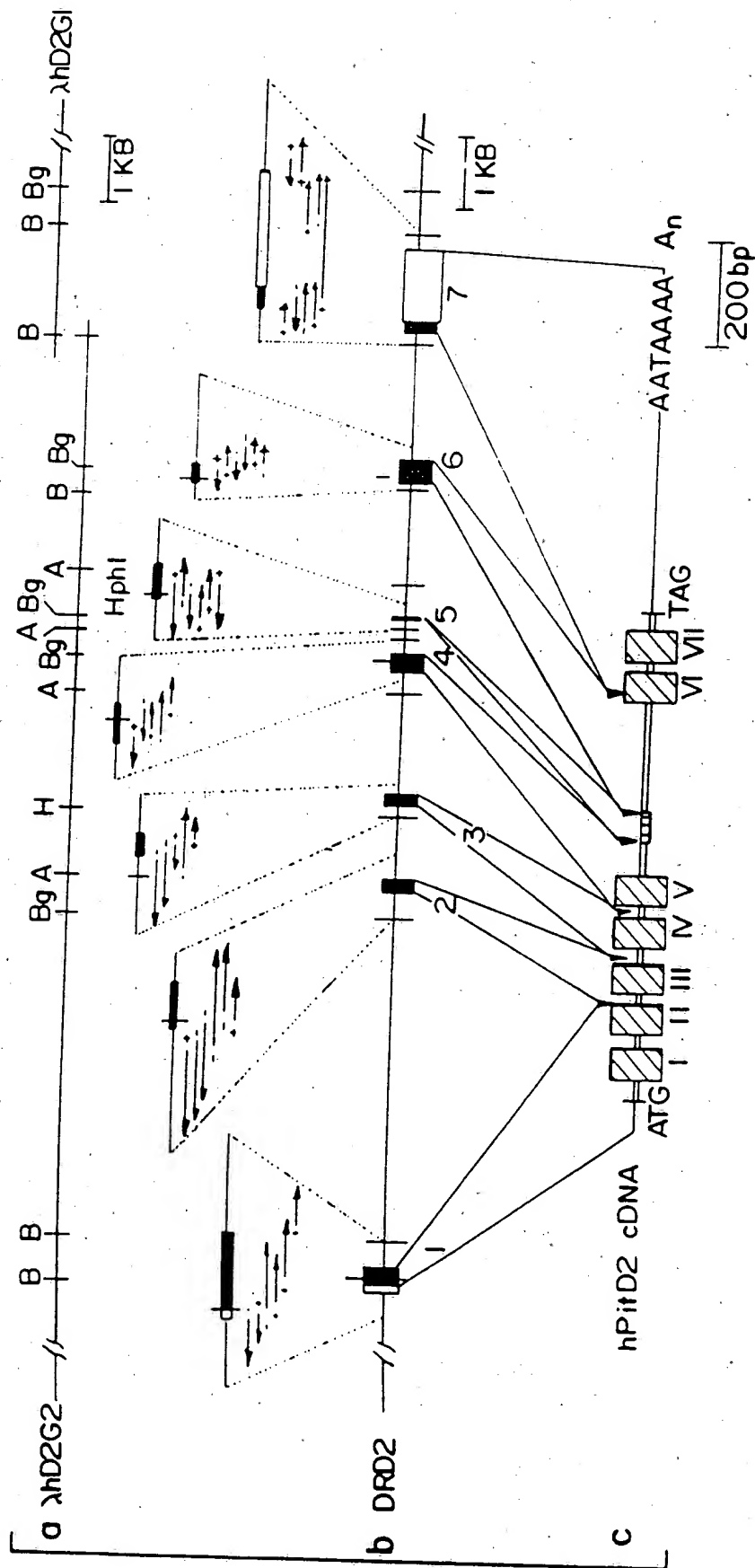
— 4.0

— 2.0

— 1.6

— 1.0

FIG. 20



DRUG	HUMAN D ₂	RAT D ₂	RAT STRIATUM
PIPERONE	0.125	0.35	0.56
(+) BUTACLAMOL	0.94	1.2	1.6
HALOPERIDOL	2.4	5.1	5.8
SULPIRIDE	206	160	205
MIANSERIN (5-HT)	2685	4300	4600
SCH 23390 (DI)	2145	2500	3300
(+) BUTACLAMOL	>10,000	>10,000	>10,000
Kd [³ H] DOMPERIDONE	0.74	0.40	0.40

FIG. 22